

K.  
Kerr

1600

#11

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/783,436

DATE: 06/03/2002

TIME: 13:59:23

Input Set : A:\Cura1721.app

Output Set: N:\CRF3\06032002\I783436.raw

p.6

ENTERED

3 <110> APPLICANT: Vernet et al.  
 5 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
 7 <130> FILE REFERENCE: 15966-672 Utility  
 9 <140> CURRENT APPLICATION NUMBER: 09/783,436  
 10 <141> CURRENT FILING DATE: 2001-02-14  
 12 <150> PRIOR APPLICATION NUMBER: 60/182,637  
 13 <151> PRIOR FILING DATE: 2000-02-15  
 15 <150> PRIOR APPLICATION NUMBER: 60/237,862  
 16 <151> PRIOR FILING DATE: 2000-10-04  
 18 <150> PRIOR APPLICATION NUMBER: 60/240,316  
 19 <151> PRIOR FILING DATE: 2000-10-13  
 21 <150> PRIOR APPLICATION NUMBER: 09/783,436  
 22 <151> PRIOR FILING DATE: 2001-02-14  
 24 <160> NUMBER OF SEQ ID NOS: 75  
 26 <170> SOFTWARE: PatentIn Ver. 2.1  
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 29 <211> LENGTH: 579  
 30 <212> TYPE: DNA  
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 36 tggggacagc aaagtctgag gactctgggtt ggtgtgggcc tgtgtgcaag gagagcagtg 180  
 37 gccatgggat aaggcctctg cacagctcta gaagcttcaa tccatttcc acccatacat 240  
 38 ctctttgtgc tctcacaccc ccacagccct tctggaataa gaccatcaca gcacagggtt 300  
 39 tgcaagatgt ctaatgccag tcattcacag ggcagctcag accctggcct gcggtgcata 360  
 40 ctaggtgact ccacatgagg tgtcatgcta gatcctgcag ggagaataag cacacacagg 420  
 41 cccgtgaccc atgctgtgga cttcatgttc taggaggtag agggagacag acaagaatca 480  
 42 aatgactgta ctaggccggg cgcactggct cagcctgta atcccagcac tttggggagg 540  
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 56 20 25 30  
 58 Thr Ala Lys Ser Glu Asp Ser Gly Trp Cys Gly Pro Val Cys Lys Glu  
 59 35 40 45  
 61 Ser Ser Gly His Gly Ile Arg Pro Leu His Ser Ser Arg Ser Phe Asn  
 62 50 55 60

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79 ctataaaaca agaaaaccctc tacgtacaga tcttttaaaa ttaaagcagg catctttgct 180
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86 gatgctcaac ccatactcag tttaccagta aaaaacata atgtttgcaa ttactcctcc 600
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101 20 25 30
103 His Glu Ile His Leu Cys Phe Ile Tyr Thr Ser Tyr Ile Tyr Ser Leu
104 35 40 45
106 Lys Val Ile Leu Tyr Ser Ile Tyr Asn Leu Ser Lys Glu Gln Ser Phe
107 50 55 60
109 Asp Cys Val Leu Thr Met Thr Arg His Val Lys Ser Tyr Val Glu Phe
110 65 70 75 80
112 Ser Thr Cys Gly Ile Thr Gln Ala Leu Lys Lys Leu Gln Ile Trp Glu
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118 Val Tyr Gln
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125 <213> ORGANISM: Homo sapiens
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128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (408)

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130 &lt;223&gt; OTHER INFORMATION: Where n is an A, T, G, or C

132 &lt;400&gt; SEQUENCE: 5

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135 cgccactgca ctccagcctg ggcgacagag cgagactccg tctcaaaaaa aaaaaaaaaa 180
136 aacatcctga gccgggctg gaaaagctct ttgcagatgg cgttccatc tctgcgcccc 240
137 tcggggtggg ggctgtccca tgttgcctc gctggggcct ctcaggtctc ctctttgccc 300
138 acccaaaagg aaaaatccac tgcacctcca cttggtgact gacgccgtgg ccagaaacat 360
W--> 139 cctggagacg ctcttccaca catggatggg gcctgctatc gatccccntg tcagctttta 420
140 tcatgccgac cagctcaagc cccaggtctc ctggatcccc aacaagcact actccggcct 480
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146 agccaggcgg gagctcctta gcctgcctgc cacctactg gctgaccagg acatcttcaa 840
147 cgctgtgacg aaggagcacc cggggctagt gcagcgtctg ccttgtgtct ggaatgtgca 900
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166 cagccccacc tatcgtgact gcctccaggc cctcaaggac gaattccacc aggacttgct 2040
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177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
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Input Set : A:\Cural721.app

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188           35           40           45
190 Pro Val Ser Phe Tyr His Ala Asp Gln Leu Lys Pro Gln Val Ser Trp
191           50           55           60
193 Ile Pro Asn Lys His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu Val
194 65           70           75           80
196 Leu Pro Asn Ala Leu Pro Ala Glu Leu Ala Arg Val Ile Val Leu Asp
197           85           90           95
199 Thr Asp Val Thr Phe Ala Ser Asp Ile Ser Glu Leu Trp Ala Leu Phe
200           100          105          110
202 Ala His Phe Ser Asp Thr Gln Ala Ile Gly Leu Val Glu Asn Gln Ser
203           115          120          125
205 Asp Trp Tyr Leu Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala
206           130          135          140
208 Leu Gly Arg Gly Phe Asn Thr Gly Val Ile Leu Leu Arg Leu Asp Arg
209 145           150          155          160
211 Leu Arg Gln Ala Gly Trp Glu Gln Met Trp Arg Leu Thr Ala Arg Arg
212           165          170          175
214 Glu Leu Leu Ser Leu Pro Ala Thr Ser Leu Ala Asp Gln Asp Ile Phe
215           180          185          190
217 Asn Ala Val Ile Lys Glu His Pro Gly Leu Val Gln Arg Leu Pro Cys
218           195          200          205
220 Val Trp Asn Val Gln Leu Ser Asp His Thr Leu Ala Glu Arg Cys Tyr
221           210          215          220
223 Ser Glu Ala Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro Lys Lys
224 225           230          235          240
226 Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Phe Tyr Leu
227           245          250          255
229 Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu Phe Val
230           260          265          270
232 Cys Pro Ser Gln Pro Pro Pro Gly Ala Glu Gln Leu Gln Gln Ala Leu
233           275          280          285
235 Ala Gln Leu Asp Glu Glu Asp Pro Cys Phe Glu Phe Arg Gln Gln Gln
236           290          295          300
238 Leu Thr Val His Arg Val His Val Thr Phe Leu Pro His Glu Pro Pro
239 305           310          315          320
241 Pro Pro Arg Pro His Asp Val Thr Leu Val Ala Gln Leu Ser Met Asp
242           325          330          335
244 Arg Leu Gln Met Leu Glu Ala Leu Cys Arg His Trp Pro Gly Pro Met
245           340          345          350
247 Ser Leu Ala Leu Tyr Leu Thr Asp Ala Glu Ala Gln Gln Phe Leu His
248           355          360          365
250 Phe Val Glu Ala Ser Pro Val Leu Ala Ala Arg Gln Asp Val Ala Tyr
251           370          375          380
253 His Val Val Tyr Arg Glu Gly Pro Leu Tyr Pro Val Asn Gln Leu Arg
254 385           390          395          400
256 Asn Val Ala Leu Ala Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser Asp

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Input Set : A:\Cural721.app

Output Set: N:\CRF3\06032002\I783436.raw

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260           420           425           430
262 Ile Glu Gln Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val Val
263           435           440           445
265 Pro Ala Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser Lys
266           450           455           460
268 Val Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe Arg
269 465           470           475           480
271 Tyr His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg Trp
272           485           490           495
274 Arg Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn Tyr Glu
275           500           505           510
277 Pro Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp Pro Arg Phe
278           515           520           525
280 Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Val Glu Leu Asp Ala
281           530           535           540
283 Gln Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala Phe Thr Ile His Leu
284 545           550           555           560
286 Pro His Ala Pro Ser Leu Asp Ile Ser Arg Phe Arg Ser Ser Pro Thr
287           565           570           575
289 Tyr Arg Asp Cys Leu Gln Ala Leu Lys Asp Glu Phe His Gln Asp Leu
290           580           585           590
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296           610           615
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307 gcgagggtcg tagtgagcca agattgtgcc actgcactcc agcctgggca acaaagttag 180
308 actcttatct tacaagaaaa aaaagaatgc ttaggaatca actcccctcc taatgcccag 240
309 acaggtgaaa tgacttgctc aggccacagt tctgcccag ccagcaccag ccagtggcac 300
310 agcagaatgc aaggagggag tggtagctac ttccacagca taggtgctgc cggggtcctc 360
311 agagcaggtg gcacagtaat aaatggcatc ccccgagtca cagcagggct tgttacaagt 420
312 cagcttgaag agcgaccagt tattctcatt gaagtggagc tcctttttct ggccgcccac 480
313 gaagaggtcc tcacatttgg ctacaaggcg ggccagggac tgggtgtaga gtccccccag 540
314 cttggcatag gtgccctcct tgetgctgat gttgctcagg agaccgtgca gctgaagctg 600
315 ggtgctcccc gtggaggcct gactggacac gctcagctgg gaggatgagg cggagggggc 660
316 ccctttgcac tggaggccag ggctcccgcg gccgcctctg ttgccgcga gccctgctgc 720
317 cggaagccag tggccctgac tttgaaagct ttctccagag gatcggaaga ggagaagaca 780
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322 <211> LENGTH: 132
323 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/783,436

DATE: 06/03/2002  
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Input Set : A:\Cural721.app  
Output Set: N:\CRF3\06032002\I783436.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:16; N Pos. 570,571,572,573,574,575,576

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Seq#:22; Xaa Pos. 274,295,296,297,298,299,300,301,302,303,304

Seq#:24; Xaa Pos. 260,261,262,263,264,265,266,267,268,269,270,271,272,273

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Seq#:75; Xaa Pos. 50